

REPLACEMENT SHEET

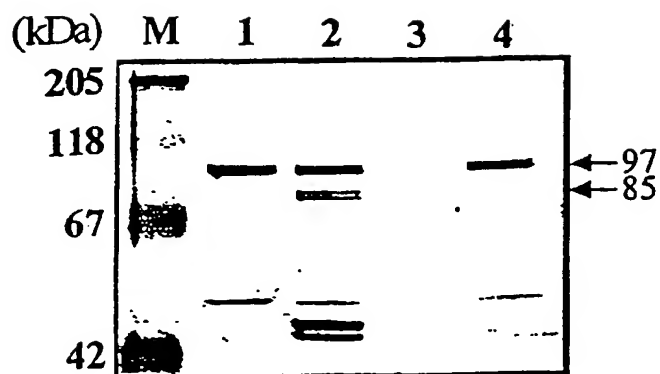


FIG.1

REPLACEMENT SHEET

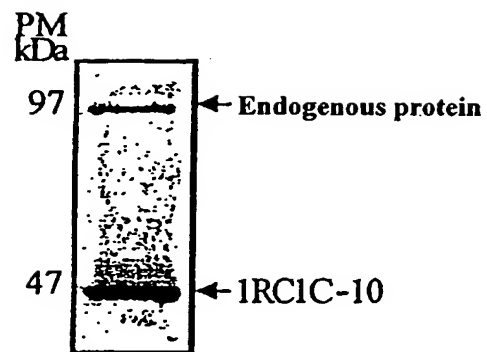


FIG. 2

REPLACEMENT SHEET

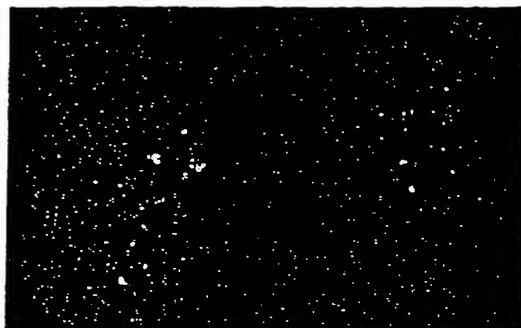


FIG. 3

REPLACEMENT SHEET



FIG. 4

REPLACEMENT SHEET

Fig. 5a

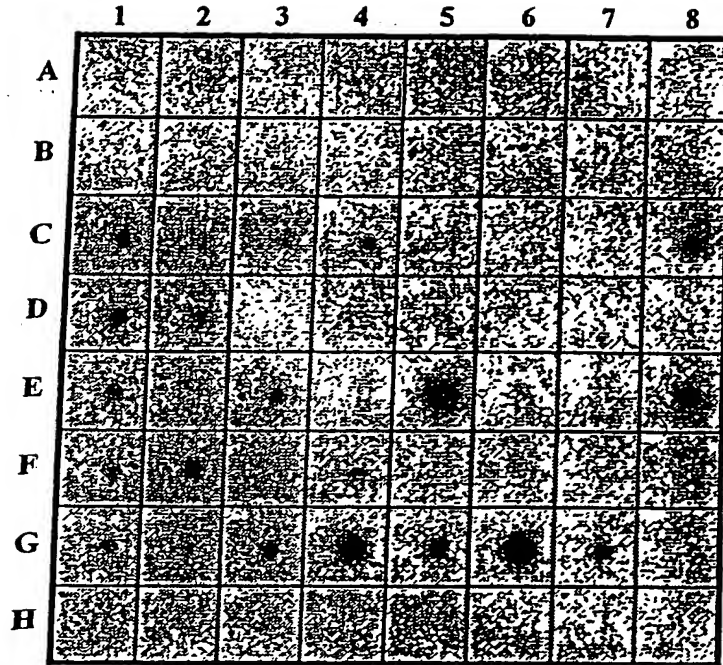


Fig. 5b

	1	2	3	4	5	6	7	8
A	whole brain	amygdala	caudate nucleus	cerebellum	cerebral cortex	frontal lobe	hippocampus	medulla oblongata
B	occipital lobe	putamen	substantia nigra	temporal lobe	thalamus	sub-thalamic nucleus	spinal cord	
C	heart	nerve	skeletal muscle	colon	bladder	uterus	prostate	stomach
D	testis	ovary	pancreas	pituitary gland	adrenal gland	thyroid gland	salivary gland	mammary gland
E	kidney	liver	small intestine	spleen	thymus	peripheral leukocyte	lymph node	bone marrow
F	appendix	lung	trachea	placenta				
G	fetal brain	fetal heart	fetal kidney	fetal liver	fetal spleen	fetal thymus	fetal lung	
H	yeast total RNA 100 ng	yeast tRNA 100 ng	E. coli rRNA 100 ng	E. coli DNA 100 ng	Poly r(A) 100 ng	human Cot1 DNA 100 ng	human DNA 100 ng	human DNA 500 ng

REPLACEMENT SHEET

1 ATGTGGATCC AGTTCGGAC CATGGATGG AGCAGACCC 40
81 GCTGAGCGG AAGATCCAGG AGCTGTCCA CGTGGAGCCA 50
161 ACGGCATAC CCTCTTCGAC TACGAGGTCC GCCTGAATGA 60
241 CACACACCA AGGAGGGGA CTCGAGCTC TCGACACCG 70
321 TCTCACCCAC GGTAGCGCG CCGCCGAGAC TGGACACAGG 80
401 TGTACAGGT CAATAGTAC GTCGATCTC CGACACAGAA 90
481 CGGAGCGCC CTTCCCGGA CGAGCCCTGC AGTCCAAGT 100
561 ATACGAGAC TACCCGGGA ACGCGTGTG CCAGATGAAC 110
641 GGCAGACCT GGAGGTGGC CAGGTGTCA TGCTCAACTA 120
721 GCGGAGATCT CCAGGAGCG CGAGACCAG ACGGCGCGG 130
801 CGACTGTGCG ATCATCTTCG TGGACGAAGT CTTCAAGATT 140
881 TGAGACGGAA GACGGGGCGG TCTGCAAGC ACTGCAAGGA 150
961 TCGGGGGCC GGCAGGACC CGACAAGCAG CTCATGTGG 160
1041 GCCCTCAGC AGTGTTCGA CGGAGACGA GTGGTACTGC 170
1121 GAGAGCGGT GAGAGAGAGC AAGAGGAATG CGAAGATGCG 180
1201 ATGGCCTGTG TGGGCGGCAC CAAGGAATGT ACCATCGTCC 190
1281 CACCNTGTG CGGTTCCGAG TCCAGGTGAG CGAGTCGGGT 200
1361 ACGAOGGATC GTACTOCCTA GTCTTGCGG GGGGCTATGA 210
1441 AGTGTGTGTC GAGATCTTTC CGGCACAAG AGGACCGGG 220
1521 GCTGGCTCTC AACTGCTTTG CTCCCATCAA TGACCAAGAA 230
1601 GGGTGTGTCG CAATGTCAAG GGTGGCAAGA ATAGCAAGTA 240
1681 GTTGTGAAT ACTGGCCCGA GAAGGGGAAG TCCGGGTTC 250
1761 TGGCCCTTGG ACGAAGGAGG GGAAGGACCG GATCAAGAG 260
1841 CCTGGCCAA CCGAGAGCGA GAGNAGGAGA ACAGCAAGAG 270
1921 AGGACGGCA AGGCCAAGTG GAAGCGGAAG TCGGCAGGAG 280
2001 GAAACCCAG GTGAGCCCT ACAGTCTCAC GCGCCAGCAG 290
2081 GGAATGAGT CCTGCGTCA CTCAGGACC GCGCGGCGAG 300
2161 AGTTTCCAGT GTATCTGCTG TCAGGAGCTG GTGTTCCGGC 310
2241 CTTGGACAGA TCTTTCGGG CACAGGTGTT GAGTGCCTT 320
2321 TGAACAGOC TCTGAGACC GTCTCTCAAC AGCTCTTCCC 330
ACACGGTGA CTCGTGTCC AGCTGACCA AGGTGGAGGA 80
GGCTGCAGA GGCTTTCTA CAGGGCAAA CAGATGGAGG 160
CACATCCAG CTCCTGGTCC GCCAGACCT COTGCTCCCC 240
ATCGGGTGT TCGCTGGCC CAGATGAGT CAGACAAGTC 320
CCAGCCCATG AGGACATGTG GAGTGAAGG GAATTGGGG 400
CATGGGGCG TGGTTTGAAG CGCAGGTGGT CAGSGTGACG 480
CCAGGCGCG GCTGGAGGAG GACGTCAATT ACCAGTGAA 560
TCCAGGAGG TCCGAGCGG CCGCCGACC ATCATCAAGT 640
CAACCCGAC AACCCCAAG AGCGGGGCT CTGTACGAC 720
AACTCTAGC CAACGTGTG CTGGGGATG ATTCTTGAA 800
GAGCGCGG GTGAAGGAG CCCCATGGT GACAACCCCA 880
CGACGTGAAC AGACTCTGA GGTCTGCG CTGCCACCTG 960
ATGAGTGGA CATGGCTTC CACATCTACT GCCTGGACCC 1040
CCTGAGTGC GGAATGATC CAGCGAGGTG GTACTGGCGG 1120
CTCGGCACA TCGTCTCTAC AGCGGACTG GGGCAAGGGC 1200
CGTCCAACA CTACGGACCC ATCCCGGGA TCCCGTGGG 1280
GTCCATCGC CCCACGTGC TGGCATCCAT GGCCGAGCA 1360
GGATGATGT GACCATGGA ATTTTTCAC ATACAGGGT 1440
AACAGTCTG TGATCAGAA CTCACCAACA CCAACAGGGC 1520
GGGGCGAGG CCAAGGACTG GCGTCTGGG AAGCGGTCA 1600
CGCCCCCGT GAGGGCAAC GCTAGGATG CATCTACAAG 1680
TCGTGTGCG CTACCTTCTG CCGAGGGAGC ATGATGAGCC 1760
CTGGGGCTGA CCATGCAGTA TCCAGAAGG TACCTGGAAG 1840
GGAAGAGGAG GAGCAGCAG AGGGGGGCTT CGCTGCCCC 1920
GTGGCCCGG CAGGGCCGG TCCCGCGCC GGCATCCAA 2000
AGCAGCTCTA TCAGAGAGA CAGAGCAAC GCCAAGCTGT 2080
CGGACGCCG TTCAGTTGT TCTGAGTAA AGTGGAGGAG 2160
CCATCACAC CTTGTGCCAG CACACGTGT GCAAGGACTG 2240
GGCTGCCGT ACGACCTGG CCGCAGCTAT GCCATGCGAG 2320
CGGCTACGG NATGGCGGT GA 2382

FIG-6

REPLACEMENT SHEET

1	HWIQVRTHDG	RQHTVDSLS	RLTKVZELRR	KIQELFHVEP	GLQRLFYRGK	QHEDGHTLFD	YEVRLNDTIQ	LLVRQSLVLP	80
81	HSTKERDSEL	SOTDSGCCIG	QSESDXSSTH	GEAAAEITDSR	PADEDMWDET	ELGLYKUNEY	VDARDTNMGA	WFEAQVVRVT	160
161	RKAPSRDEPC	SSTSRPALEE	DVIYHVKYDD	YPENGVVQMN	SROVRARART	IIKWQDLEVG	QVWHLNPNPD	NPKERGFWYD	240
241	AEISRKRETR	TARELYANVV	LGDDSLNDCR	IIFVDEVFKI	ERPGEGSPMV	DNPHRRKSOP	SCHCKRDDVN	RLCKVCACHL	320
321	CGGRQDPDKQ	LMCDECDMAF	HIYCLDPPLS	SVPSEDEWYC	PECRNDASEV	VLAGERLRES	KKNAKMASAT	SSSQRDWGRG	400
401	MACVGRTEKC	TIVPSNHYGP	IPGIPVGTMW	RFRVQVSESG	VHRPHVAGIH	GRSNDGSYSL	VLAGGYEDDV	DHGNFFTYTG	480
481	SGGRDLSGNK	RTAEQSCDQK	LTNTNRALAL	NCFAPINDQE	GAEAKDWRSQ	KPVRVVRNVK	GGKNSKYAPA	EGNRYDGIYK	560
561	VVKYMPKGRK	SGFLVMRYLL	RRODDEPGPW	TREGKDRIRK	LGLTMQYPEG	YLEALANRR	EKENSKEEEE	EQQEGGFASP	640
641	ATGKGWKRK	SAGGGSRSAG	SPRRTSKTKK	VEPYSLTAQQ	SSLIREDKSN	AKLMNEVLAS	LKDRPASGSP	FQLFLSKVEE	720
721	TFQCICQCEL	VFRPITTVCC	HNVCRCCLDR	SFRAQVFSCP	ACRYDLORSY	AHQVNQPLQT	VLNQLFPGYG	NGR*	794

FIG-7

REPLACEMENT SHEET

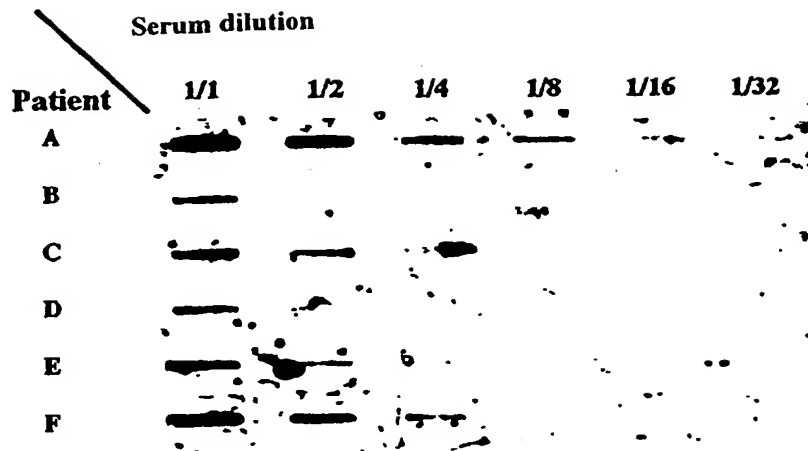
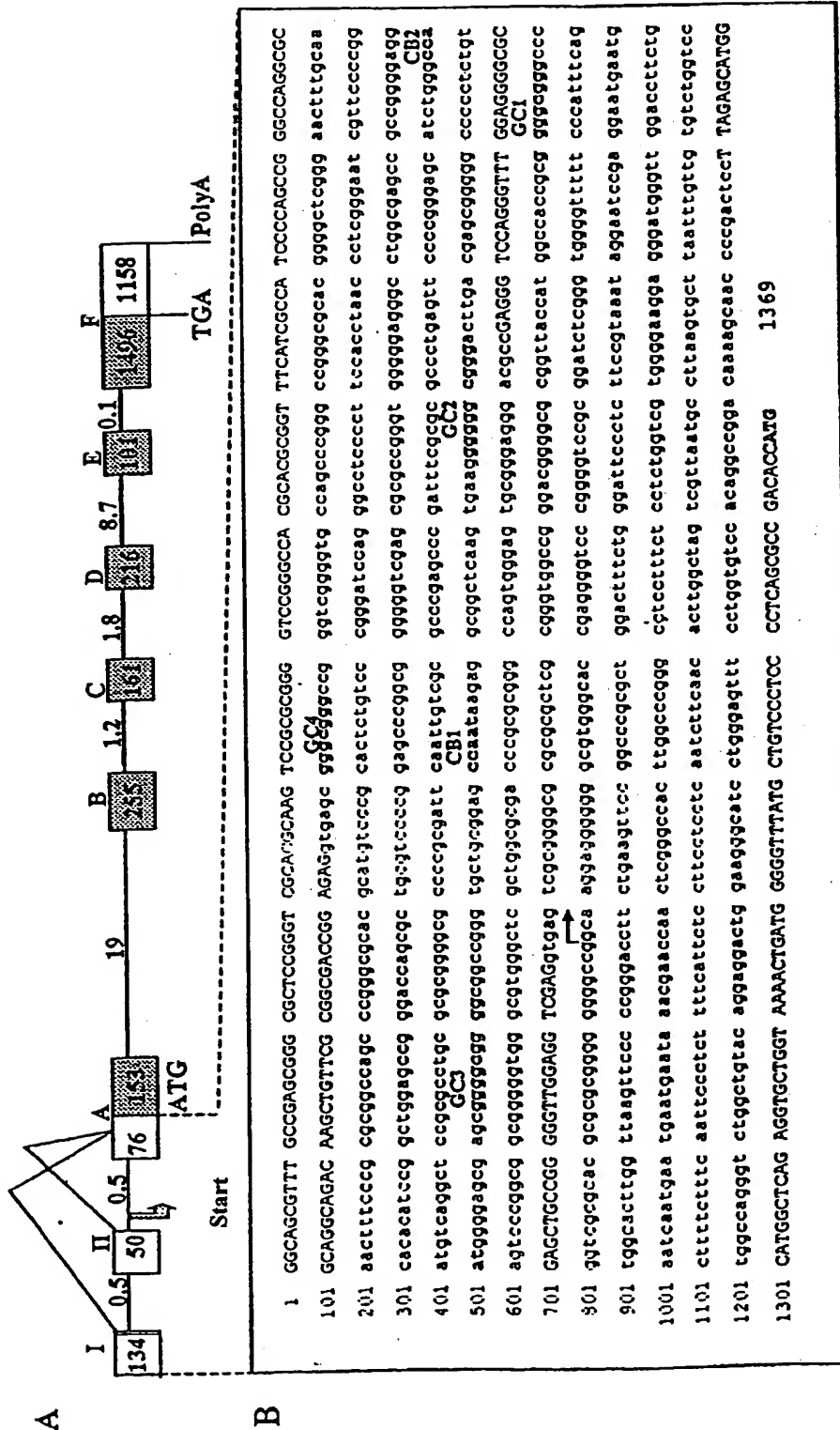


FIG-8

REPLACEMENT SHEET

FIG-9



REPLACEMENT SHEET

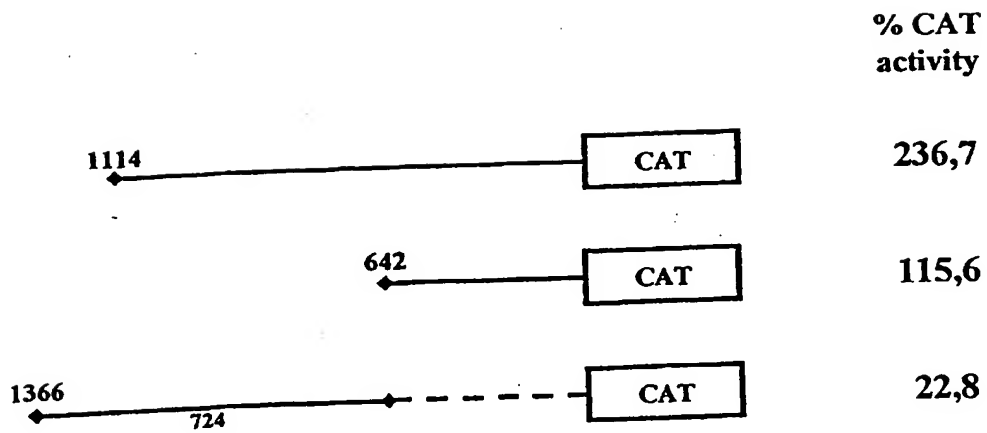


FIG 10

REPLACEMENT SHEET

FIG-11A

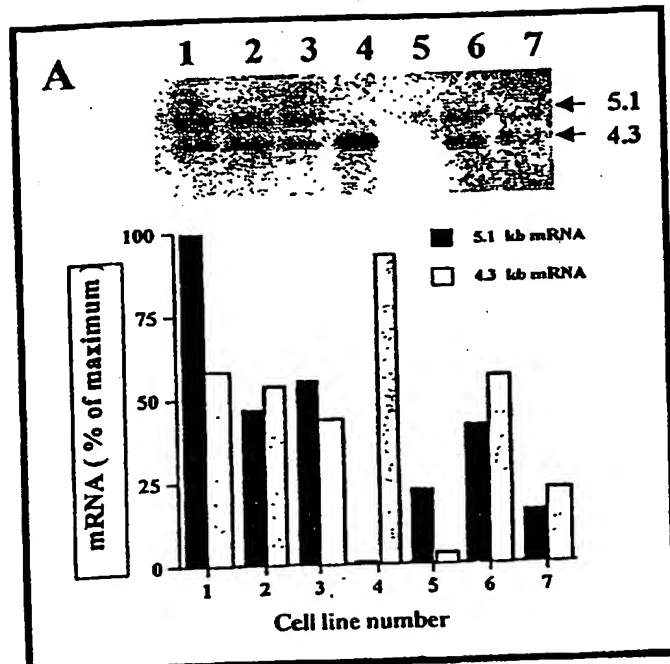


FIG-11B

